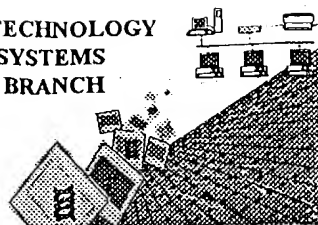


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/840,2770

Source: FW16

Date Processed by STIC: 9/15/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~  
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/849,2770

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos        was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                               prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering                use space characters, instead.
  
- 4      Non-ASCII            The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
     J                         ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s) <sup>15</sup> contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
                               each n or Xaa can only represent a single residue. Please present the maximum number of each  
                               residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                    sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the  
                               previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                               the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
                               Artificial or Unknown sequences.
  
- 7      Skipped Sequences    Sequence(s) \_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                               (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               This sequence is intentionally skipped  
  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences    Sequence(s) \_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)            <210> sequence id number  
                               <400> sequence id number  
                               000
  
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)            Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                               In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>        Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response                scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or  
                               is Artificial Sequence
  
- 11      Use of <220>        Sequence(s) \_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
                               Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                               "Unknown." Please explain source of genetic material in <220> to <223> section.  
                               (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                               listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

## RAW SEQUENCE LISTING

DATE: 09/15/2004

PATENT APPLICATION: US/09/840,277D

TIME: 09:25:05

Input Set : A:\A-688A.ST25.txt

Output Set: N:\CRF4\09152004\I840277D.raw

3 <110> APPLICANT: FEIGE, ULRICH  
 4 KOHNO, TADAHIKO  
 5 LACEY, DAVID  
 6 BOONE, THOMAS CHARLES  
 8 <120> TITLE OF INVENTION: ADHESION ANTAGONISTS (as amended)  
 10 <130> FILE REFERENCE: A-688A  
 12 <140> CURRENT APPLICATION NUMBER: US 09/840,277D  
 13 <141> CURRENT FILING DATE: 2001-04-23  
 15 <150> PRIOR APPLICATION NUMBER: US 60/198,919  
 16 <151> PRIOR FILING DATE: 2000-04-21  
 18 <150> PRIOR APPLICATION NUMBER: US 60/201,394  
 19 <151> PRIOR FILING DATE: 2000-05-03  
 21 <160> NUMBER OF SEQ ID NOS: 137  
 23 <170> SOFTWARE: PatentIn version 3.2  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 684  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Homo sapiens  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (1)..(684)  
 35 <400> SEQUENCE: 1  
 36 atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg 48  
 37 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu  
 38 1 5 10 15  
 40 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc 96  
 41 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 42 20 25 30  
 44 atg atc tcc ccg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc 144  
 45 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 46 35 40 45  
 48 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag 192  
 49 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 50 50 55 60  
 52 gtg cat aat gcc aag aca aag ccg ccg gag gag cag tac aac agc acg 240  
 53 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 54 65 70 75 80  
 56 tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat 288  
 57 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 58 85 90 95  
 60 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc 336  
 61 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 62 100 105 110

Does Not Comply  
Corrected Diskette Needed

5-7

## RAW SEQUENCE LISTING

DATE: 09/15/2004

PATENT APPLICATION: US/09/840,277D

TIME: 09:25:05

Input Set : A:\A-688A.ST25.txt

Output Set: N:\CRF4\09152004\I840277D.raw

```

64 atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag      384
65 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
66      115      120      125
68 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc      432
69 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
70      130      135      140
72 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg      480
73 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
74 145      150      155      160
76 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      528
77 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
78      165      170      175
80 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc      576
81 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
82      180      185      190
84 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      624
85 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
86      195      200      205
88 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      672
89 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
90      210      215      220
92 tct ccg ggt aaa      684
93 Ser Pro Gly Lys
94 225
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 228
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
104 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
105 1      5      10      15
108 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
109      20      25      30
112 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
113      35      40      45
116 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
117      50      55      60
120 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
121 65      70      75      80
124 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
125      85      90      95
128 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
129      100      105      110
132 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
133      115      120      125
136 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
137      130      135      140
140 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
141 145      150      155      160

```

## RAW SEQUENCE LISTING

DATE: 09/15/2004

PATENT APPLICATION: US/09/840,277D

TIME: 09:25:05

Input Set : A:\A-688A.ST25.txt

Output Set: N:\CRF4\09152004\I840277D.raw

```

144 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
145                               165                               170                               175
148 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
149                               180                               185                               190
152 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
153                               195                               200                               205
156 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
157                               210                               215                               220
160 Ser Pro Gly Lys
161 225
164 <210> SEQ ID NO: 3
165 <211> LENGTH: 8
166 <212> TYPE: PRT
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: Preferred linker
172 <400> SEQUENCE: 3
174 Gly Gly Gly Lys Gly Gly Gly Gly
175 1 5
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 8
180 <212> TYPE: PRT
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Preferred linker
186 <400> SEQUENCE: 4
188 Gly Gly Gly Asn Gly Ser Gly Gly
189 1 5
192 <210> SEQ ID NO: 5
193 <211> LENGTH: 8
194 <212> TYPE: PRT
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Preferred linker
200 <400> SEQUENCE: 5
202 Gly Gly Gly Cys Gly Gly Gly Gly
203 1 5
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 5
208 <212> TYPE: PRT
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Preferred linker
214 <400> SEQUENCE: 6
216 Gly Pro Asn Gly Gly
217 1 5
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 5
222 <212> TYPE: PRT

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/840,277D

DATE: 09/15/2004

TIME: 09:25:05

Input Set : A:\A-688A.ST25.txt

Output Set: N:\CRF4\09152004\I840277D.raw

```

223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Laminin peptide
228 <400> SEQUENCE: 7
230 Tyr Ile Gly Ser Arg
231 1 5
234 <210> SEQ ID NO: 8
235 <211> LENGTH: 49
236 <212> TYPE: PRT
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Echistatin peptide
242 <400> SEQUENCE: 8
244 Glu Cys Glu Ser Gly Pro Cys Cys Arg Asn Cys Lys Phe Leu Lys Glu
245 1 5 10 15
248 Gly Thr Ile Cys Lys Arg Ala Arg Gly Asp Asp Met Asp Asp Tyr Cys
249 20 25 30
252 Asn Gly Lys Thr Cys Asp Cys Pro Arg Asn Pro His Lys Gly Pro Ala
253 35 40 45
256 Thr
260 <210> SEQ ID NO: 9
261 <211> LENGTH: 7
262 <212> TYPE: PRT
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: RGD, NGR derivative peptide
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <222> LOCATION: (2, 5 and)..(7)
272 <223> OTHER INFORMATION: Xaa is any amino acid
274 <400> SEQUENCE: 9
W--> 276 Arg Xaa Glu Thr Xaa Trp Xaa
277 1 5
280 <210> SEQ ID NO: 10
282 <400> SEQUENCE: 10
W--> 283 000
285 <210> SEQ ID NO: 11
286 <211> LENGTH: 9
287 <212> TYPE: PRT
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: RGD, NGR derivative peptide
294 <220> FEATURE:
295 <221> NAME/KEY: misc_feature
296 <222> LOCATION: (2, 3, 7 and)..(8)
297 <223> OTHER INFORMATION: Xaa is any amino acid
299 <400> SEQUENCE: 11
W--> 301 Cys Xaa Xaa Arg Leu Asp Xaa Xaa Cys
302 1 5

```

## RAW SEQUENCE LISTING

DATE: 09/15/2004

PATENT APPLICATION: US/09/840,277D

TIME: 09:25:05

Input Set : A:\A-688A.ST25.txt

Output Set: N:\CRF4\09152004\I840277D.raw

305 <210> SEQ ID NO: 12  
 307 <400> SEQUENCE: 12  
 W--> 308 000  
 310 <210> SEQ ID NO: 13  
 311 <211> LENGTH: 9  
 312 <212> TYPE: PRT  
 313 <213> ORGANISM: Artificial Sequence  
 315 <220> FEATURE:  
 316 <223> OTHER INFORMATION: RGD, NGR derivative peptide  
 319 <220> FEATURE:  
 320 <221> NAME/KEY: misc\_feature  
 321 <222> LOCATION: (1, 2, 3, 7, 8 and)..(9)  
 322 <223> OTHER INFORMATION: Xaa is any amino acid with Xaa at 1, 3, 7 and 9 capable of  
 323 forming a bridge.  
 325 <400> SEQUENCE: 13  
 W--> 327 Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa  
 328 1 5  
 331 <210> SEQ ID NO: 14  
 332 <211> LENGTH: 17  
 333 <212> TYPE: PRT  
 334 <213> ORGANISM: Artificial Sequence  
 336 <220> FEATURE:  
 337 <223> OTHER INFORMATION: RGD, NGR derivative peptide  
 340 <220> FEATURE:  
 341 <221> NAME/KEY: misc\_feature  
 342 <222> LOCATION: (2, 3, 4, 5, 6, 12, 13, 14, 15 and)..(16)  
 343 <223> OTHER INFORMATION: At positions 2, 3, 4, 5, 6, 12, 13, 14, 15 and 16, Xaa is  
 any  
 344 amino acid or may be absent.  
 346 <400> SEQUENCE: 14  
 W--> 348 Cys Xaa Xaa Xaa Xaa Xaa Cys Arg Gly Asp Cys Xaa Xaa Xaa Xaa Xaa  
 349 1 5 10 15  
 352 Cys  
 356 <210> SEQ ID NO: 15  
 357 <211> LENGTH: 8  
 358 <212> TYPE: PRT  
 359 <213> ORGANISM: Artificial Sequence  
 361 <220> FEATURE:  
 362 <223> OTHER INFORMATION: RGD, NGR derivative peptide  
 365 <220> FEATURE:  
 366 <221> NAME/KEY: misc\_feature  
 367 <222> LOCATION: (1 and)..(8)  
 368 <223> OTHER INFORMATION: Xaa is an independently selected amino acid.  
 370 <220> FEATURE:  
 371 <221> NAME/KEY: misc\_feature  
 372 <222> LOCATION: (2 and)..(7)  
 373 <223> OTHER INFORMATION: Xaa equals 0 to 4 amino acids, each which is independently  
 374 selected.  
 376 <220> FEATURE:  
 377 <221> NAME/KEY: misc\_feature

(see p. 6)

09/840,277D 6

<210> 15  
<211> 8  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> RGD, NGR derivative peptide

FST

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

same error in sequence 16.

<220>  
<221> misc\_feature  
<222> (1 and) .. (8)  
<223> Xaa is an independently selected amino acid.



<220>  
<221> misc\_feature  
<222> (2 and) .. (7)  
<223> Xaa equals 0 to 4 amino acids, each which is independently selected.

variable length is not permitted.

<220>  
<221> misc\_feature  
<222> (4) .. (4)  
<223> Xaa is selected from the group consisting of glycine and leucine.

Xaa can only represent a single amino acid.

<220>  
<221> misc\_feature  
<222> (5) .. (5)  
<223> Xaa is selected from the group consisting of tryptophan and leucine.

(see item 5 on Error Summary Sheet)

<400> 15

what about Xaa at location 6?

Xaa Xaa Asp Asp Xaa Xaa Xaa Xaa  
1 5



RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/840,277D

DATE: 09/15/2004  
TIME: 09:25:06

Input Set : A:\A-688A.ST25.txt  
Output Set: N:\CRF4\09152004\I840277D.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. ~~2,5,7~~  
Seq#:11; Xaa Pos. ~~2,3,7,8~~  
Seq#:13; Xaa Pos. ~~1,2,3,7,8,9~~  
Seq#:14; Xaa Pos. ~~2,3,4,5,6,12,13,14,15,16~~  
Seq#:15; Xaa Pos. ~~1,2,5,6,7,8~~  
Seq#:16; Xaa Pos. 1,2,3,6,7,8,9,10  
Seq#:17; Xaa Pos. 3,5,6,13,15  
Seq#:18; Xaa Pos. 2,3,4,7,15  
Seq#:19; Xaa Pos. 3,4,5,6,8,13,15,18  
Seq#:20; Xaa Pos. 2,5,6,7,12,13,14  
Seq#:21; Xaa Pos. 1,3,6,9,12,13  
Seq#:40; Xaa Pos. 3,4  
Seq#:50; Xaa Pos. 2,3  
Seq#:58; Xaa Pos. 5  
Seq#:59; Xaa Pos. 6  
Seq#:86; Xaa Pos. 3,15  
Seq#:87; Xaa Pos. 13,15

**VERIFICATION SUMMARY**

DATE: 09/15/2004

PATENT APPLICATION: US/09/840,277D

TIME: 09:25:06

Input Set : A:\A-688A.ST25.txt

Output Set: N:\CRF4\09152004\I840277D.raw

L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
L:283 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:  
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
L:308 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:  
L:327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0  
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0  
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0  
L:481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0  
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0  
M:341 Repeated in SeqNo=19  
L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0  
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0  
L:817 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0  
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0  
L:1109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0  
L:1129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0  
L:1525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0  
L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0